Untitled

```
Title:
                     US- 10- 578- 672A- 1
Perfect score:
                    191
Sequence:
                     1 ggt gt ggaggt gt t caaagg..... gacact aaat t gt ggat aat 191
RESULT 5
AAS69177
LD
      AAS69177 standard; cDNA; 1431 BP.
XX
AC
       AAS69177:
13-FEB-2002 (first entry)
       DNA encoding novel human diagnostic protein #4981.
       Human; chromosome mapping; gene mapping; gene therapy; forensic;
       food supplement; medical imaging; diagnostic; genetic disorder; ss.
      Homo sapi ens.
      WC200175067- A2.
       11- OCT- 2001.
       30-MAR-2001; 2001WO-US008631.
       31- MAR- 2000: 2000US- 00540217.
       23- AUG- 2000; 2000 US- 00649167.
(HYSE-) HYSEQ INC.
       Drmanac RT, Liu C, Tang YT;
       WPI: 2001-639362/73.
       P-PSDB: ABG04990.
       New isolated polynucleotide and encoded polypeptides, useful in
       diagnostics, forensics, gene mapping, identification of mutations
       responsible for genetic disorders or other traits and to assess
       bi odi ver si t y.
       Claim 1; SEQ ID NO 4981; 103pp; English.
       The invention relates to isolated polynucleotide (I) and polypeptide (II)
      sequences. (1) is useful as hybrid sation probes, polymerase chain reaction (PCA) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used
       in diagnostics as expressed sequence tags for identifying expressed
      genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
       supplement. (II) and its binding partners are useful in medical imaging
       of sites expressing (II). (I) and (II) are useful for treating disorders
       involving aberrant protein expression or biological activity.
       polypeptide and polynucleotide sequences have applications in
      diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
       coding sequences of the invention. Note: The sequence data for this
       patent did not appear in the printed specification, but was obtained in
       electronic format directly from WIPO at
       ftp. wipo.int/pub/published pct sequences
                                                     Page 1
```

Untitled

```
Sequence 1431 BP; 391 A; 346 C; 383 G; 311 T; 0 U; 0 Other;
  Query Match 83.0% Score 158.6; DB 5; Length 1431; Best Local Similarity 89.9% Pred. No. 2.4e-36;
                                  0: M smatches
  Matches 170: Conservative
                                                     19:
                                                         Indel s
                                                                     0: Gaps
                                                                               0:
             3 TGTGGAGGTGTTCAAAGGCATTGACAATCGGACTCAGAAAGTAGTCGCCATAAAAATCAT 62
Qy
          183 TGGAGAGGTGTTCAAAAGCATTGACAATCGGACTCAGAAAGTGGTTGCCATAAAGATCAT 242
Db
           63 TGACCTGGACGACGCACAACATCACATCGACGACATTCACCACGAAATCACACTGCTGAC 122
Qy
          243 TGATCTGGAAGAAGCTGAAGATGAGATAGAGCACATTCAACAAGAAATCACAGTGCTGAG 302
Db
Qv
          123 TCAGTGTGACAGTCCCTACGTAACCAAATATTACGGATCCTACCTGAAGGACACTAAATT 182
          303 TCAGTGTGACAGTCCATATGTAACCAAATATTATGGATCCTATCTGAAGCATACAAAATT 362
Dh
          183 GTGGATAAT 191
Qy
          363 ATGGATAAT 371
Dh
                 US- 10- 578- 672A- 1
Title:
Perfect score:
                191
Sequence:
                 1 ggt gt ggaggt gt t caaagg......gacact aaat t gt ggat aat 191
RESULT 37
ACH38568
     ACH38568 standard; cDNA; 472 BP.
XX
ACH38568:
     13-OCT-2003 (first entry)
     Human endothelial cell cDNA #6701.
     Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
     genome mapping; biodiversity; genetic disorder.
     Homo sapiens.
     US2003073623- A1.
     17- APR- 2003.
     30-JUL-2001; 2001US-00918995.
     30-JUL-2001: 2001US-00918995.
XX
PA
     (DRMA/) DRMANAC R.T.
PA
     (LABA/) LABAT I
     (STAC/) STACHE- CRAIN B.
(DICK/) DICKSON M.C.
PA
PA
PA
     (JONE/) JONES L W
XX
ΡĬ
     Dr.manac RT. Labat I. Stache-Orain B. Dickson MC. Jones LW.
ХX
```

Page 2

Untitled

DR WPI: 2003-615964/58. XX New polynucleotide sequences obtained from various cDNA libraries, useful ΡŤ as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. Claim 1; SEQ ID NO 25780; 44pp; English. The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for POR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or FNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdat a. uspt o. gov/ sequence. ht ml ?Doc1 D=20030073623 Sequence 472 BP; 149 A; 91 C; 119 G; 110 T; 0 U; 3 Other; Query Match 16.8% Score 32; DB 10; Length 472; Fred. No. 6.6e-06; Best Local Similarity 100.0% 32; Conservative 0; M smatches Gaps Mat ches 0: Indel s 0: 0: Qy 106 GAAATCACAGTGCTGAGTCAGTGTGACAGTCC 137 178 GAAATCACAGTCCTGAGTCAGTGTGACAGTCC 209 Db